Spatial Epidemiology of Dengue and Leptospirosis in Sri Lanka: A Geospatial Analysis of Disease Clustering and Hotspots

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Dengue and leptospirosis are significant vector-borne and zoonotic diseases that impose a considerable public health burden in Sri Lanka. Although their prevalence is well documented, understanding their distinct spatial patterns at a sub-national level is essential for effective resource allocation and targeted interventions. This study aims to identify, analyze, and compare the spatial distributions and hotspots of dengue and leptospirosis across Sri Lanka's 25 districts. District-level monthly aggregated case data were analyzed using multiple spatial statistical techniques. Global spatial autocorrelation was assessed using Getis-Ord Global G and Global Moran's I statistics. Local clustering patterns were identified using Local Indicators of Spatial Association (LISA) and Getis-Ord Gi* hotspot analysis. Additionally, spatial regression models, namely the Spatial Lag Model (SLM) and Spatial Durbin Model (SDM), were applied to evaluate the influence of climatic variables, including average rainfall and temperature. Results reveal significantly different spatial distributions between the two diseases. Dengue exhibited strong local clustering, with Kernel Density Estimation (KDE) identifying a dominant hotspot in the highly urbanized Western Province. Global Moran's I for dengue showed significant positive spatial autocorrelation (3.250, $p = 0.000675$), indicating clustering of similar values. However, the Getis-Ord Global G statistic was not significant (-0.8412, $p = 0.7999$), suggesting a complex pattern driven by localized clusters of both high and low values. Outside the Western Province, most districts did not exhibit statistically significant hotspot or cold spot patterns. In contrast, leptospirosis showed strong global clustering, supported by both Global Moran's I (5.0178, $p = 0$) and Getis-Ord Global G (2.0997, $p = 0.0178$). Spatial Lag Model results indicated rainfall as a significant positive predictor for both diseases, with stronger influence on leptospirosis ($\beta = 0.764$, $p < 0.001$) compared to dengue ($\beta = 0.570$, $p = 0.011$). Hotspot analysis identified significant leptospirosis clusters in southern districts such as Kalutara, Galle, Matara, and Hambantota, characterized by high rainfall and agricultural activity, while northern regions showed cold spots. Overall, dengue and leptospirosis exhibit distinct, non-random spatial patterns influenced by different risk factors. Dengue is strongly associated with urbanization, whereas leptospirosis is linked to agro-climatic conditions. These findings highlight the importance of spatial statistical tools in developing targeted, disease-specific public health strategies.

Keywords: dengue, leptospirosis, spatial, clustering, hotspots, coldspots